

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:30:32 ; Search time 23.63 Seconds

(Without alignments)
658.146 Million cell updates/sec

Title: US-09-653-755A-4

Perfect score: 2427

Sequence: 1 EVQLOQSGELVKPGASVMI.....RHEGLKNLYLKRTISPK 454

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1802	74.2	336	1 GCB_MOUSE	P01866 mus musculu
2	1797	74.0	405	1 GCBM_MOUSE	P01867 mus musculu
3	1419	58.5	330	1 GCAA_MOUSE	P01865 mus musculu
4	1414	58.3	339	1 GCAB_MOUSE	P01864 mus musculu
5	1385.5	57.1	335	1 GCB_MOUSE	P20761 rattus norv
6	1326.5	54.7	333	1 GCB_MOUSE	P20762 rattus norv
7	1202.5	49.5	329	1 GCB_MOUSE	P22436 mus musculu
8	1170	48.2	329	1 GCB_MOUSE	P03987 mus musculu
9	1159	47.8	329	1 GCB_MOUSE	P01866 mus musculu
10	1150	47.4	324	1 GCB_MOUSE	P01865 mus musculu
11	1145	47.2	333	1 GCB_MOUSE	P01869 rattus norv
12	1112	45.8	326	1 GCB_MOUSE	P20760 rattus norv
13	1100	45.3	322	1 GCB_MOUSE	P01857 homo sapien
14	1087	44.8	330	1 GCB_MOUSE	P01870 oryctolagus
15	1080.5	44.5	323	1 GCB_MOUSE	P01862 cavia porce
16	1080.5	44.5	323	1 GCB_MOUSE	P01863 mus musculu
17	1059	43.6	326	1 GCB_MOUSE	P01853 homo sapien
18	1054.5	43.4	327	1 GCB_MOUSE	P01861 homo sapien
19	776.5	32.0	290	1 GCB_MOUSE	P01871 homo sapien
20	478	19.7	454	1 GCB_MOUSE	P01875 mus musculu
21	477.5	19.7	429	1 GCB_MOUSE	P06336 mus musculu
22	474	19.5	421	1 GCB_MOUSE	P01854 mus musculu
23	473	19.5	428	1 GCB_MOUSE	P06336 mus musculu
24	462	19.0	418	1 GCB_MOUSE	P01853 mus musculu
25	457.5	18.9	417	1 GCB_MOUSE	P01756 mus musculu
26	457.5	18.9	417	1 GCB_MOUSE	P01757 mus musculu
27	443.5	18.3	438	1 GCB_MOUSE	P23085 heterodontu
28	436.5	18.0	370	1 GCB_MOUSE	P23087 heterodontu
29	431.5	17.8	438	1 GCB_MOUSE	P23088 heterodontu
30	431	17.8	438	1 GCB_MOUSE	P23088 heterodontu
31	431	17.8	438	1 GCB_MOUSE	P23088 heterodontu
32	430.5	17.7	120	1 GCB_MOUSE	P01747 mus musculu
33	429.5	17.7	136	1 GCB_MOUSE	P01755 mus musculu

ALIGNMENTS

RESULT	1	STANDARD	PRT	336 AA.
GCB_MOUSE				
ID	GCB_MOUSE			
AC	P01866;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	IG GAMMA-2B CHAIN C REGION.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (A ALLELE)			
RX	MEDLINE=80120716; PubMed=6766534;			
RA	Yanawaki-Kataoka Y., Kataoka T., Takahashi N., Odata M., Honjo T.;			
RT	"Complete nucleotide sequence of immunoglobulin gamma2b chain gene			
RT	cloned from newborn mouse DNA."			
RL	Nature 283:786-789(1980).			
RN	[2]			
RP	SEQUENCE FROM N.A. (MPC 11).			
RX	MEDLINE=80081501; PubMed=117548;			
RA	Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;			
RT	"Structure of the constant and 3' untranslated regions of the murine			
RT	gamma 2b heavy chain messenger RNA."			
RL	Science 206:1299-1303(1979).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=80081502; PubMed=117549;			
RA	Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;			
RT	"Sequence of the cloned gene for the constant region of murine gamma			
RT	2b immunoglobulin heavy chain."			
RL	Science 206:1303-1306(1979).			
RN	[4]			
RP	SEQUENCE FROM N.A. (B ALLELE)			
RX	MEDLINE=82173203; PubMed=6803173;			
RA	Olio R., Rougeon F.;			
RT	"Mouse immunoglobulin allotypes: post-duplication divergence of gamma			
RT	2a and gamma 2b chain genes."			
RL	Nature 296:761-763(1982).			
RN	[5]			
RP	CARBOHYDRATE-LINKAGE SITE THR-105.			
RX	MEDLINE=94216359; PubMed=7512967;			
RA	Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.;			
RT	Irimura T., Takahashi N., Kato K., Arata Y.;			
RT	"O-glycosylation in hinge region of mouse immunoglobulin G2b."			
RL	J. Biol. Chem. 269:12345-12350(1994).			
CC	-1- PPM: O-LINKED GLYCANS CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS			
CC	MODIFIED WITH 2 SIALIC ACID RESIDUES.			
CC	-1- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA			
CC	CHAINS.			
CC	-1- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.			
DR	PIR: A02157; GZMS11.			
DR	InterPro: IPR000495; -			
DR	InterPro: IPR003006; -			
DR	Pfam: PF00047; 19; 3.			

34	429	17.7	391	1	MUCB_HUMAN	P04220 homo sapien
35	426.5	17.6	393	1	HVC3_HETFR	P23086 heterodontu
36	421.5	17.4	461	1	HVCN_HETFR	P23088 heterodontu
37	421	17.3	479	1	MOCM_RABIT	P04221 oryctolagus
38	420	17.3	457	1	MOC_CANFA	P01874 canis famli
39	417	17.2	450	1	MOC_SUNMU	P20768 suncus mur
40	416.5	17.2	140	1	HV02_MOUSE	P01746 mus musculu
41	416	17.1	137	1	HV11_MOUSE	P01755 mus musculu
42	405	16.7	117	1	HV14_MOUSE	P01758 mus musculu
43	402.5	16.6	353	1	ALC1_GORGO	P20758 gorilla gor
44	401	16.5	120	1	HV50_MOUSE	P06329 mus musculu
45	396.5	16.3	138	1	HV48_MOUSE	P03980 mus musculu

OY 419 MKTSKWEKTDSPSCNVREHGLKNYLLKTKTISRSPG 453
 DB 301 MKTSKWEKTDSPSCNVREHGLKNYLLKTKTISRSPG 335

RESULT 3
 GCAM_MOUSE STANDARD; PRT: 330 AA.

AC P01863; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 IG GAMMA-2A CHAIN C REGION, A ALLELE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81076554; PubMed=6777755;
 RA Sikorav J.-L., Auffray C., Rougeon F.;
 RT "Structure of the constant and 3' untranslated regions of the murine
 RT Balb/c gamma 2a heavy chain messenger RNA.";
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81198976; PubMed=6262729;
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 RT and evolution of heavy chain genes: further evidence for intervening
 RT sequence-mediated domain transfer.";
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81223894; PubMed=6787604;
 RA Olio R., Auffray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic
 RT family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RX MEDLINE=74175517; PubMed=4831970;
 RA Bourgois A., Fougereau M., Rocca-Serra J.;
 RT "Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
 RT for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435(1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=73056887; PubMed=4565406;
 RA de Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma G2a
 RT immunoglobulin. Identification of the disulfide bridges.";
 RL Eur. J. Biochem. 30:452-462(1972).

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DR EMBL: V00798; CAA24178.1; -;
 DR PIR: A02152; G2MSA.
 DR InterPro: IPR000495; -;
 DR InterPro: IPR003006; -;
 DR Pfam: PF00047; 19; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT MOD_RES 330 330
 SQ SEQUENCE 330 AA; 36389 MM; B84361C5445A6864 CRC64; REMOVED POST-TRANSLATIONALLY.

Query Match 58.5%; Score 1419; DB 1; Length 330;
 Best Local Similarity 78.6%; Pred. No. 5.9e-92;
 Matches 264; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

OY 119 AKTTPPSVPLAPGCGDTTSSVTLGCLYKGFPSVVTWNSSGLSSVTFPALDSG 178
 DB 1 AKTTPASVYPLAPVCGDITSSVTLGCLYKGFPEPVLTLNNSGSLSGVTFPVLQSD 60

OY 179 LYTSSSVTPSPSTWPSOTVCSVAHPASSSTTPYDKLEPSPISTINPCPCCKCPCPA 238
 DB 61 LYTSSSVTPSTWPSOTVCSVAHPASSSTTPYDKLEPSPISTINPCPCCKCPCPA 114

OY 239 PNLGGPSVFTFPPIKIVLMISLTPKVTGVVYDSEDDPVOQSMFVNNEVHTAQTQT 298
 DB 115 PNLGGPSVFTFPPIKIVLMISLTPKVTGVVYDSEDDPVOQSMFVNNEVHTAQTQT 174

OY 299 HREDYNSTIRVSTLPIODHMSGKFKCVNNKDLPSLERTSKTKGLVRAQVYTL 358
 DB 175 HREDYNSTIRVSTLPIODHMSGKFKCVNNKDLPSLERTSKTKGLVRAQVYTL 234

OY 359 PPPAEOLSRKQVSLTCLVGVNPGDISVEWTSNGTSENYDPAVLNDSYFYSLTN 418
 DB 235 PPPAEOLSRKQVSLTCLVGVNPGDISVEWTSNGTSENYDPAVLNDSYFYSLTN 294

OY 419 MKTSKWEKTDSPSCNVREHGLKNYLLKTKTISRSPG 454
 DB 295 VEKKWVRNRSYSCSVHAGLHNHTTSPSRTPK 330

RESULT 4
 GCAM_MOUSE STANDARD; PRT: 399 AA.

AC P01865; 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.

CC -I- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
 CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
 CC THE A ALLELE.

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CC -----

DR EMBL: J00471: AAB59661.1: ALT_INIT.

DR PIR: A02154: G2MSAB.

DR MGD: MGI:96443: Igh-1.

DR InterPro: IPR000495: -.

DR InterPro: IPR003006: -.

DR Pfam: PF00047: Iy: 3.

DR PROSITE: PS00290: IG_MHC: 1.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KM Transmembrane; Alternative splicing.

FT NON_TER 1 1

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 144 204

FT DISULFID 250 308

FT TRANSMEM 346 363

FT DOMAIN 364 399

FT CARBOHYD 180 180

FT SEQUENCE 399 AA: 44020 MW: 4C38138BFAED3FE0 CRC64;

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 58.3%; Score 1414; DB 1; Length 399;

Best local Similarity 78.5%; Pred. No. 1.7e-91;

Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

QY 119 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYPESVYTWNSGLSSSVHTEPALLOSG 178

DB 1 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYPESVYTWNSGLSSSVHTEPALLOSG 60

QY 179 LYTMSSSVTPSPSTQSVAPASSTVDKLEPESGISTINPCPKCKECHKCPA 238

DB 61 LYTMSSSVTPSPSTQSVAPASSTVDKLEPESGISTINPCPKCKECHKCPA 114

QY 239 PNLGGPSVFIIPPNIKDVLMISLPKVCVYVDVSEDDPDVQISFVNVNVEVHTAQOT 298

DB 115 PNLGGPSVFIIPPNIKDVLMISLPKVCVYVDVSEDDPDVQISFVNVNVEVHTAQOT 174

QY 299 HREDYSTRVVSALPIQHDMMGSKFEKCKVNNKDLPSPIERTISKIGLYRAPQVYL 358

DB 175 HREDYSTRVVSALPIQHDMMGSKFEKCKVNNKDLPSPIERTISKIGLYRAPQVYL 234

QY 359 PPBAELSRKDVSLTCLVYGFNPDISVETNSGHTENKQAPVLDSDGSYFIYSKLN 418

DB 235 PPBAELSRKDVSLTCLVYGFNPDISVETNSGHTENKQAPVLDSDGSYFIYSKLN 294

QY 419 MKTSKWEKTDSEFCNVRHGLKNYLYLKTISRSPG 453

DB 295 VEKKNNVERNSYSCSVYHGLNHHHTTKSRIRPG 329

RESULT 5

GCAB_MOUSE STANDARD: PRT: 335 AA.

ID GCAB_MOUSE P01864:

AC 21-JUL-1986 (rel. 01, Created)

DT 21-JUL-1986 (rel. 01, Last sequence update)

DT 15-JUL-1999 (rel. 38, Last annotation update)

DE IG GAMMA-2A CHAIN C REGION, B ALLELE.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RX MEDLINE=82037861; PubMed=6170065;

RT Schreier P.H., Botwell A.L.M., Mueller-Hill B., Baltimore D.;

"Multiple differences between the nucleic acid sequences of the

RT IgG2a and IgG2b alleles of the mouse.";

RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).

RN [2]

RP SEQUENCE.

RA MEDLINE=82037777; PubMed=6794027;

RT Dognin M.J., Lauwereys M., Strosberg A.D.;

RT "Multiple amino acid substitutions between murine gamma 2a heavy

chain Fc regions of Ig1a and Ig1b allotypic forms";

RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

CC - MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,

FROM BALB/C MICE, AT 156 OF THE POSITIONS.

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CC EMBL: J00479: -; NOT_ANNOTATED_CDS.

DR PIR: A02153: G2MSAB.

DR InterPro: IPR000495: -.

DR InterPro: IPR003006: -.

DR Pfam: PF00047: Iy: 3.

DR PROSITE: PS00290: IG_MHC: 1.

KM Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1 1

FT SEQUENCE 335 AA: 36596 MW: FA3382792CB13C6 CRC64;

Query Match 57.1%; Score 1385.5; DB 1; Length 335;

Best local Similarity 77.1%; Pred. No. 1.3e-89;

Matches 259; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

QY 119 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYPESVYTWNSGLSSSVHTEPALLOSG 178

DB 1 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYPESVYTWNSGLSSSVHTEPALLOSG 60

QY 179 LYTMSSSVTPSPSTQSVAPASSTVDKLEPESGISTINPCPKCKECHKCPA 238

DB 61 LYTMSSSVTPSPSTQSVAPASSTVDKLEPESGISTINPCPKCKECHKCPA 119

QY 239 PNLGGPSVFIIPPNIKDVLMISLPKVCVYVDVSEDDPDVQISFVNVNVEVHTAQOT 298

DB 120 PNLGGPSVFIIPPNIKDVLMISLPKVCVYVDVSEDDPDVQISFVNVNVEVHTAQOT 179

QY 299 HREDYSTRVVSALPIQHDMMGSKFEKCKVNNKDLPSPIERTISKIGLYRAPQVYL 358

DB 180 HREDYSTRVVSALPIQHDMMGSKFEKCKVNNKDLPSPIERTISKIGLYRAPQVYL 239

QY 359 PPBAELSRKDVSLTCLVYGFNPDISVETNSGHTENKQAPVLDSDGSYFIYSKLN 418

DB 240 PPBAELSRKDVSLTCLVYGFNPDISVETNSGHTENKQAPVLDSDGSYFIYSKLN 299

QY 419 MKTSKWEKTDSEFCNVRHGLKNYLYLKTISRSPG 454

DB 300 VQKSTWERSLFCACSVYHGLNHHHTTKISRSLCK 335

RESULT 6

GCAB_MOUSE STANDARD: PRT: 333 AA.

ID GCAB_MOUSE P20761:

AC 01-FEB-1991 (rel. 17, Created)

DT 01-FEB-1991 (rel. 17, Last sequence update)

DT 15-JUL-1999 (rel. 38, Last annotation update)

DE IG GAMMA-2B CHAIN C REGION.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018;
DR InterPro; IPR000495; -
DR InterPro; IPR003006; -
DR Pfam; PF00047; 1g; 3;
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 15
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D8D460A6 CRC64;

Query Match 54.7%; Score 1326.5; DB 1; Length 333;
Best Local Similarity 73.6%; Pred. No. 1.6e-85;
Matches 248; Conservative 34; Mismatches 50; Indels 5; Gaps 3;

QY 119 AKTPPSVYPLAPGCGDGTSSVTGLCLVKGYFPEPSVTYVWNSGSLSSVHTFPALLQSG 178
1 AQTAPSVYPLAPGCGDGTSSVTGLCLVKGYFPEPSVTYVWNSGSLSSVHTFPALLQSG 60
DB 1 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVKLE-PSGPSTINPCPPCKECHKCP 237
179 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVKLE-PSGPSTINPCPPCKECHKCP 237
DB 61 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVKLE-PSGPSTINPCPPCKECHKCP 116
238 APNLEGGSVFIFPPNIDVIMISLTPKVCYVVDSEDDPDVOISFVNNVEVHTAQTQ 297
DB 117 VPELLGGSVFIFPPKPKDILLISQNAKVTVCYVDSEEDPDVOISFVNNVEVHTAQTQ 176
QY 298 THREDYNTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 357
177 PREEDYNTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 236
DB 177 PREEDYNTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 236
QY 358 LPPAEQLSRKDVSLTCLVGFNPEDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 417
DB 237 MGPPEQLTEGTVALTCLTSGFLPNDIGEVWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 296
QY 418 MKTSKWEKTDSPSCNVREHGLKNYLLKKTISRSPGK 454
DB 297 NVERSKWDSPAPFCVYHEGLAHNHAVEKISRPPGK 333

RESULT 7
GCC_RAT STANDARD; PRT; 329 AA.
ID GCC_RAT
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2C CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galifre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07189; CAA30169.1; -
DR PIR; S00847; S00847.
DR InterPro; IPR000495; -
DR InterPro; IPR003006; -
DR Pfam; PF00047; 1g; 3;
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCDD7B7933850773 CRC64;

Query Match 49.5%; Score 1202.5; DB 1; Length 329;
Best Local Similarity 68.2%; Pred. No. 7e-77;
Matches 229; Conservative 35; Mismatches 65; Indels 7; Gaps 4;

QY 119 AKTPPSVYPLAPGCGDGTSSVTGLCLVKGYFPEPSVTYVWNSGSLSSVHTFPALLQSG 178
1 ARTAPSVYPLAPGCGDGTSSVTGLCLVKGYFPEPSVTYVWNSGSLSSVHTFPALLQSG 60
DB 1 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVKLE-PSGPSTINPCPPCKECHKCP 238
179 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVKLE-PSGPSTINPCPPCKECHKCP 238
DB 61 LYTSSSVTVSSVMPSTQVTCVAHPASSSTTVKLE-PSGPSTINPCPPCKECHKCP 114
239 PNLEGGSVFIFPPNIDVIMISLTPKVCYVVDSEDDPDVOISFVNNVEVHTAQTQ 298
DB 115 DNL-GRPSVFIFPPKPKDILLISQNAKVTVCYVDSEEDPDVOISFVNNVEVHTAQTQ 173
QY 299 HREDYNTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 358
DB 174 HEEQLNGTFRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAQYVI 233
QY 359 PPPAEQLSRKDVSLTCLVGFNPEDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 418
DB 234 PPPAEQLSRKDVSLTCLVGFNPEDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 293
QY 419 MKTSKWEKTDSPSCNVREHGLKNYLLKKTISRSPGK 454
DB 294 VDTDSWMDGDIYTCVYHEGLAHNHHTQKNLSRSPGK 329

RESULT 8
GCC_MOUSE STANDARD; PRT; 329 AA.
ID GCC_MOUSE
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

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RA Tucker P.W., Blattner F.R.;
RT *Structural analysis of the murine IgG3 constant region gene.*;
RL EMBL J. 3:2041-2046(1984).
CC -----
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CC -----
CC EMBL: J00451; NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR InterPro: IPR000495;
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin C region; Glycoprotein; Transmembrane;
KW Alternative splicing.
FT NON_TER 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 48.2%; Score 1170; DB 1; Length 329;
Best Local Similarity 66.2%; Pred. No. 1.3e-74;
Matches 221; Conservative 33; Mismatches 74; Indels 6; Gaps 1;

QY 121 TTPPSVYPLAPGCGDTGSSVTGCLVKGYPESVVTWNSSGSLSSVHTFPALLQSGLY 180
DB 2 TTPASVYPLVPGSGDSITGSSVTLGCLVKGFPPEVTVKNNYGLSSGRTVSSVLQSGFY 61
QY 181 TMSSTVTVSSSTWPSQTVTCVAHPASSTVDKLEPSGISTINPCPPCKECHKCPAPN 240
DB 62 SLSSLTVTSSSTWPSQTVTCVAHPASSTVDKLEPSGISTINPCPPCKECHKCPAPN 115
QY 241 LREGPSVFTFPPIKDVLMISLTPKVTGVVDSEDDPDVQISMFVNNVHTAQTQTR 300
DB 116 ILGGPSVFTFPPIKDVLMISLTPKVTGVVDSEDDPDVQISMFVNNVHTAQTQTR 175
QY 301 EDYNSIRVSVTLPIOHOMMSGKEFKCKVNNKDLPSPIERTISIKGLVRAPOVYITLP 360
DB 176 AOVNSTFRVSAALPIOHOMMRGKEFKCKVNNKALPAPERTISIKGKAQTPOVYITIP 235
QY 361 PAEOLSRKDVSLTCLVAVGNPDISVEMTNGHTEENYKDTAPVLDSDGSYFIYSKLNMK 420
DB 236 PREOMSKKKVSLTCLVNTNFSEALISVEMERNGELEDYKNTPIILSDGTYFLYSKLTVD 295
QY 421 TSKWEKTDSEFCNVNRHGLKNTYLLKKTISRSPCK 454
DB 296 TDSWLQGEIFTCVVAHEALHNHTQKNLSRSPCK 329

RESULT 9
GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

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RA Tucker P.W., Blattner F.R.;
RT *Structural analysis of the murine IgG3 constant region gene.*;
RL EMBL J. 3:2041-2046(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00451; AAB59655.1; ALT_SEQ.
DR PIR: A02156; G3MSM.
DR InterPro: IPR000495;
DR InterPro: IPR003006;
DR Pfam: PF00047; Ig; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 47.8%; Score 1159; DB 1; Length 398;
Best Local Similarity 66.0%; Pred. No. 9.5e-74;
Matches 219; Conservative 33; Mismatches 74; Indels 6; Gaps 1;

QY 121 TTPPSVYPLAPGCGDTGSSVTGCLVKGYPESVVTWNSSGSLSSVHTFPALLQSGLY 180
DB 2 TTPASVYPLVPGSGDSITGSSVTLGCLVKGFPPEVTVKNNYGLSSGRTVSSVLQSGFY 61
QY 181 TMSSTVTVSSSTWPSQTVTCVAHPASSTVDKLEPSGISTINPCPPCKECHKCPAPN 240
DB 62 SLSSLTVTSSSTWPSQTVTCVAHPASSTVDKLEPSGISTINPCPPCKECHKCPAPN 115
QY 241 LREGPSVFTFPPIKDVLMISLTPKVTGVVDSEDDPDVQISMFVNNVHTAQTQTR 300
DB 116 ILGGPSVFTFPPIKDVLMISLTPKVTGVVDSEDDPDVQISMFVNNVHTAQTQTR 175
QY 301 EDYNSIRVSVTLPIOHOMMSGKEFKCKVNNKDLPSPIERTISIKGLVRAPOVYITLP 360
DB 176 AOVNSTFRVSAALPIOHOMMRGKEFKCKVNNKALPAPERTISIKGKAQTPOVYITIP 235
QY 361 PAEOLSRKDVSLTCLVAVGNPDISVEMTNGHTEENYKDTAPVLDSDGSYFIYSKLNMK 420
DB 236 PREOMSKKKVSLTCLVNTNFSEALISVEMERNGELEDYKNTPIILSDGTYFLYSKLTVD 295
QY 421 TSKWEKTDSEFCNVNRHGLKNTYLLKKTISRSP 452
DB 296 TDSWLQGEIFTCVVAHEALHNHTQKNLSRSP 327

RESULT 10
GC1_MOUSE

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ID	GC1.MOUSE	STANDARD:	PRT:	324 AA.
AC	P01668;			
DT	21-JUL-1986 (rel. 01, Created)			
DT	21-JUL-1986 (rel. 01, Last sequence update)			
DT	30-MAY-2000 (rel. 39, Last annotation update)			
DE	IG GAMMA-1 CHAIN C REGION.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=80045036; PubMed=115593;			
RA	Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,			
RA	Takahashi N., Mano Y.;			
RT	"Cloning and complete nucleotide sequence of mouse immunoglobulin			
RT	gamma 1 chain gene.";			
RL	Cell 18:559-568(1979).			
RN	[2]			
RN	SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).			
RX	MEDLINE=80202559; PubMed=6769752;			
RA	Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,			
RA	Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;			
RT	"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences			
RT	cloned in a bacterial plasmid.";			
RL	Gene 9:87-97(1980).			
RL	[3]			
RP	SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).			
RX	MEDLINE=80012837; PubMed=113776;			
RA	Rogers J., Clarke P., Salser W.;			
RT	"Sequence analysis of cloned cDNA encoding part of an immunoglobulin			
RT	heavy chain.";			
RL	Nucleic Acids Res. 6:3305-3321(1979).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN MOPC 21).			
RX	MEDLINE=78242288; PubMed=98524;			
RA	Aderuugo K.;			
RT	"Evolution of immunoglobulin subclasses. Primary structure of a			
RT	murine myeloma gammal chain.";			
RL	J. Biol. Chem. 253:6068-6075(1978).			
RN	[5]			
RP	DISULFIDE BONDS (MOPC 21).			
RX	MEDLINE=73008889; PubMed=5073237;			
RA	Svaeti J., Milstein C.;			
RT	"The disulphide bridges of a mouse immunoglobulin G1 protein.";			
RL	Biochem. J. 126:837-850(1972).			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL, V00793; CAA24172.1; -			
DR	EMBL, V00793; CAA24173.1; -			
DR	EMBL, V00793; CAA24174.1; -			
DR	EMBL, V00793; CAA24175.1; -			
DR	EMBL, V00793; CAA24176.1; -			
DR	PIR, A02159; GIMS.			
DR	GLYCOSITEDB; P01868; -			
DR	MGD; MGI:96446; Igh-4.			
DR	InterPro; IPR000495; -			
DR	InterPro; IPR003006; -			
DR	PIfam; PF00047; Ig; 3.			
KW	PROSITE; PS00290; IG_MHC; 1.			
KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;			
KW	Alternative splicing.			
FT	NON_TER	1		
FT	DOMAIN	1	97	CH1.
FT	DOMAIN	98	110	HINGE.
FT	DOMAIN	111	217	CH2.

FT	DOMAIN	218	324	CH3
FT	DISULFID	27	82	
FT	DISULFID	102	102	INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID	104	104	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	107	107	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	109	109	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	138	198	
FT	CARBOHYD	174	174	N-LINKED (GLCNAC. . .).
FT	DISULFID	244	302	
FT	MOD_RES	324	324	REMOVED POST-TRANSLATIONALLY.
FT	CONFLICT	276	276	N -> D (IN REF. 3).
FT	CONFLICT	278	278	N -> D (IN REF. 3).
SO	SEQUENCE	324 AA;	35704 MW;	A338812F3D1F2C93 CRC64;

Query Match 47.4%; Score 1150; DB 1; Length 324;
Best Local Similarity 64.6%; Pred. No. 3.1e-73;
Matches 217; Conservative 45; Mismatches 62; Indels 12; Gaps 4;

QY	119	AKTTPSPVYPLAPGCGDTGGSSVTGLCLVKGFPESVTVTNWSSGSSVHTFPALLQSG	178
Db	1	AKTTPSPVYPLAPGSAQTNSMVLTVGLVKGFPETVTVTNWSSGSSGSHVTFPAVLQSD	60
QY	179	LYTMSSSTVTVSSSTWPSQTVTCVAHPASSSTTVDKLPESGFISTINCPCKECKHKCPA	238
Db	61	LYTLSSSTVTVSSSPSETVTCVAHPASSSTTVDKKIVP-----RDC-GCKPC-ICTV	111
QY	239	PNLEGGSPVFLEPPPIKIKVIMISLTPKTCVVDVSEDDPDVYQPMVNNVEVHRAQTOT	298
Db	112	PEVS---SVLEFPKPKVYLTITLTKTCVVDISKDDPEYQSFVDDVEVHRAQTOT	168
QY	299	HREDYNSTRVSTLPLOHODMWSGCKEKKCNKNDLPSPIERTISKIGLVARAOVYL	358
Db	169	REDEQNSFRSRSSELPIMHODMLNKEKRCRNSAAPAPLEKTSIKRGRKARQVYTI	228
QY	359	PPPAQLSKRVDLSLCLVYVGNPDGISVEMTNSNGHTEENYKDFAPVLDSDGSYPIYSKLN	418
Db	229	PPPKQMAKDKVLSLCLMTITDFEPEDITYEMQMNGQPAENYKNTOPIMNTNGSFYYSKLN	288
QY	419	MKTSKWEKTSDFSCNVHREGLKNLYLKLTISRSPEK	454
Db	289	VQKSNWEAGNFTCSVLHGLNHTTEKSLSHSPEK	324

RESULT 11
GCIM_MOUSE STANDARD; PRT; 393 AA.

ID	GCIM_MOUSE	STANDARD	PRT	393 AA.
AC	P01869;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	IG GAMMA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.			
OS	Mus musculus (Mouse).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=68045036; PubMed=115593;			
RA	Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,			
RA	Takahashi N., Mano Y.,			
RT	"Cloning and complete nucleotide sequence of mouse immunoglobulin			
RL	gamma 1 chain gene.";			
RL	Cell 18:559-568(1979).			
RN	[2]			
RP	SEQUENCE OF 323-393 FROM N.A.			
RX	MEDLINE=82197625; PubMed=6804503;			
RA	Tyler B.M., Cowman A.F., Gerodakis S.D., Adams J.M., Bernard O.,			
RT	"mRNA for surface immunoglobulin gamma chains encodes a highly			
RT	conserved transmembrane sequence and a 28-residue intracellular			
RL	domain.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).			
RN	[3]			

RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 RT immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
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 CC -----
 CC EMBL: V00793; CAA24172.1; -
 DR EMBL: V00793; CAA24173.1; -
 DR EMBL: V00793; CAA24174.1; -
 DR PIR: B02159; GIMSM.
 DR MGD: MGI:96446; Igh-4.
 DR InterPro: IPR000495; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Iq; 3.
 DR ProSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane.
 FT NON-TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT DISULFID 244 302
 FT TRANSMEM 340 357
 FT DOMAIN 358 393 POTENTIAL.
 FT SEQUENCE 393 AA; 43386 MW; 4CC8343B7A1CE27 CRC64; CYTOPLASMIC (POTENTIAL).
 Query Match 47.2%; Score 1145; DB 1; Length 393;
 Best Local Similarity 64.5%; Pred. No. 8.8e-73;
 Matches 216; Conservative 45; Mismatches 62; Indels 12; Gaps 4;
 QY 119 AKTTPPSVPLAPGCGDTGSSVTLGCLVKGTFPESVYVYTNSSGSSSVHTFPALQSG 178
 DB 1 AKTTPPSVPLAPGSAQNSMTLGLCLVKGTFPEVYVYTNSSGSSSVHTFPALQSD 60
 QY 179 LYTMSSTVVPSTPSTQVTCVSAHPASTVYDKKLEPESGISTINTNCPPECKEHCPC 238
 DB 61 LYTLLSSVVPSTPSTQVTCVSAHPASTVYDKKLEPESGISTINTNCPPECKEHCPC 238
 QY 239 PNLGEGPSVFIFPPNPKIDVLMISLPKVTYCVVVDSEDDPDVQISWFNVNEVHTAQTQT 298
 DB 112 PEVTS---SVFIFPPKPKVDLTITLPKVTYCVVVDISKDDPEVQISWFNVDVDEVHTAQTQT 168

QY 299 HREDYNSITRVSTLPIQHODMWSGKEFKCKYNNKDLPSPIERTISKGLVAPQVYL 358
 DB 169 REQGFNSTFRSVSELPIMQDMLNGKEFKCRVNSAAPPRIEKTISKTKGRKARQVYI 228
 QY 359 PPPEQLSRKRDVSLCLVYGVNPGDISVEMTSNGHTEENYKDTAPVLDSDGSFYISKLN 418
 DB 229 PPPEQMKARDKSLTLCMTIDFPEDITEVMQNGQPAENYKKTQPIMTNNGSYFYISKLN 288
 QY 419 MKTSKWEKTDSPSCNVRHGLKNYILAKTISRSPG 453
 DB 289 YQKSNMEAGNFTCVSLHGLHNHTEKSLSHSPG 323
 RESULT 12
 ID GCL_RAT STANDARD; PRT; 326 AA.
 AC P20759;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Buelegemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR: PS0017; PS0017.
 DR InterPro: IPR000495; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Iq; 3.
 DR ProSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 KW Non-ter 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;
 Query Match 45.8%; Score 1112; DB 1; Length 326;
 Best Local Similarity 61.9%; Pred. No. 1.4e-70;
 Matches 208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;
 QY 119 AKTTPPSVPLAPGCGDTGSSVTLGCLVKGTFPESVYVYTNSSGSSSVHTFPALQSG 178
 DB 1 AKTTPPSVPLAPGSAQNSMTLGLCLVKGTFPEVYVYTNSSGSSSVHTFPALQSD 60
 QY 179 LYTMSSTVVPSTPSTQVTCVSAHPASTVYDKKLEPESGISTINTNCPPECKEHCPC 238
 DB 61 LYTLLSSVVPSTPSTQVTCVSAHPASTVYDKKLEPESGISTINTNCPPECKEHCPC 238
 QY 239 PNLGEGPSVFIFPPNPKIDVLMISLPKVTYCVVVDSEDDPDVQISWFNVNEVHTAQTQT 298
 DB 114 SEVTS---SVFIFPPKPKVDLTITLPKVTYCVVVDISKDDPEVQISWFNVDVDEVHTAQTQT 170
 QY 299 HREDYNSITRVSTLPIQHODMWSGKEFKCKYNNKDLPSPIERTISKGLVAPQVYL 358
 DB 171 PEQGFNSTFRSVSELPILHODMLNGRFRCKVTSAPSPSEIKTISKDEGRTQVPHYVTM 230

QY 359 PPAEOLSRKDVSLTCLVGVFNPBGDISVEMTNSNGHTEENYKDTAPVLDSDGSFYLYSKLN 418
 DB 231 SPTKEMTONEYSITCMWKGFFPPDIYEMWQNGOPQOEYKNTPTMTDGDGSFYLYSKLN 290
 QY 419 MKTSKMEKTDSPSCNVHRHGLKNLYLKRTISRSRPGK 454
 DB 291 VAKEMKOGNFTGCSVLHGLHNHHTKSLSHSPGK 326

RESULT 13

GCA_RAT ID GCA_RAT STANDARD: PRT: 322 AA.
 AC P20760:
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2A CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RL "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
 CC -----
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 CC -----
 CC EMBL: M13804; AAA41376.1; ALT_INIT.
 DR PIR: PS0019; PS0019.
 DR InterPro: IPR000495; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 19; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 136 196
 FT DISULFID 242 300
 FT CARBOHYD 172 172 N-LINKED (GLUCNAC. .) (POTENTIAL).
 SO SEQUENCE 322 AA; 35186 MW; EBEAL136A9DE01EDB CRC64;

Query Match 45.3%; Score 1100; DB 1; Length 322;
 Best Local Similarity 60.4%; Pred. No. 9.3e-70;
 Matches 203; Conservative 53; Mismatches 66; Indels 14; Gaps 2;

QY 119 AKTTPSYVPLAPGCGDPTGSSVTGLGVKGFPESSVTYTNMGSLSSTVHTFPALQSG 178
 DB 1 AETTAPSYVPLAPGATLAKNSMTVIGCLVKGFFPEYTYTNMGSLSSTVHTFPALQSG 60
 QY 179 LYTMSSSVTVBSSWPSQTVTCVAHPASSSTTVDKKLEPSGPISTINPCPCKECHKCPA 238
 DB 61 LYTLTSSVTBSSWSSOAVTCNVAHPASSSTVKDKKIYP-----RECNPCCG 107
 QY 239 PNLLEGSPVFETPPNKKVYLMSTLPKTYCYVVDSEDDPDVQISFVNNVHYHTAQOTF 298
 DB 108 TGSEVVS-SVETFPPTKDVLTTLTPKTYCYVVDISQNDPEVRFSGFTIDVEVHTAQOTHA 166
 QY 299 HREDNSTIRVYSTLPIDHODMWSGKEFKCKVNNKDLPSIRRTSKIKGLVRAPOVYTL 358
 : |||:| ||| |||:| ||| |||:| ||| |||:| ||| |||:| ||| |||:

DB 167 PEKQNSTLRVSELPYVHRDLNKGTFCKYVNSGAFPAPIEKSISKEPGRGPOVYTM 226
 QY 359 PPAEOLSRKDVSLTCLVGVFNPBGDISVEMTNSNGHTEENYKDTAPVLDSDGSFYLYSKLN 418
 DB 227 APPKEEMTQSOVSIQCMWKGFFPPDIYEMWQNGOPQOEYKNTPTMTDGDGSFYLYSKLN 286
 QY 419 MKTSKMEKTDSPSCNVHRHGLKNLYLKRTISRSRPGK 454
 DB 287 VAKETWQGNFTGCSVLHGLHNHHTKSLSHSPGK 322

RESULT 14

GCL_HUMAN ID GCL_HUMAN STANDARD: PRT: 330 AA.
 AC P01857;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 GN IGHG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82274238; PubMed=6287432;
 RA Ellison J.W., Berson B.J., Hood L.E.;
 RL "The nucleotide sequence of a human immunoglobulin C gamma1 gene."; Nucleic Acids Res. 10:4071-4079(1982).
 RN [2]
 RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
 RX MEDLINE=71064024; PubMed=5489771;
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.;
 RL "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).
 RN [3]
 RP SEQUENCE OF 136-329 (EU).
 RX MEDLINE=71064025; PubMed=5530842;
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., Edelman G.M.;
 RL "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; Biochemistry 9:3171-3181(1970).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN NIE).
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponslingl H., Hilschmann N.;
 RL "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; Hoppe-seyler's Z. physiol. Chem. 357:1571-1604(1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RL "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; Hoppe-seyler's Z. physiol. Chem. 364:713-747(1983).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RL "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."; Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 DR Dreker L., Schwarz J., Reichel W., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal
 RT 19G1 immunoglobulin (myeloma protein M μ), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanoagen bromide cleavage products, and the disulfide bridges."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8].
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE-81208100; PubMed-7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9 and 2.8-A resolution."
 RL Biochemistry 20:2361-2370(1981).
 CC -I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 CC -----
 DR EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A02146; GHU.
 DR PDB: 1RC1; 15-JUL-92.
 DR PDB: 1RC2; 15-JUL-92.
 DR MIM: 147100; -.
 DR InterPro: IPR000495; -.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; 19; 3.
 DR PROSITE: PS00290; IG_MHC. 2.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 99 110 CH1.
 FT DOMAIN 111 223 HINGE.
 FT DOMAIN 224 330 CH2.
 FT DISULFID 27 83 CH3.
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 183 197
 FT TURN 198 199
 N-LINKED (GLCNAC. . .).
 REMOVED POST-TRANSLATIONALLY.
 K -> R (IN GIM(3) MARKER).
 D -> E (IN GIM(NON-1) MARKER).
 /FTID-VAR_003887.
 L -> M (IN GIM(NON-1) MARKER).
 /FTID-VAR_003888.

FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SO SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA3D CRC64;
 Query Match 44.8%; Score 1087; DB 1; Length 330;
 Best Local Similarity 60.8%; Pred. No. 7; 7e-69;
 Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;
 QY 119 AKTPPSVYPLAGCCDDTGGSSVTLCGLKGYPRESEVTYTWNGSSLSSSHHPALLO-S 177
 DB 1 ASKKGSSVPLPSSKSTSGGTALGLVKDFPEPVTWSNGALTSVGHFPALQSS 60
 QY 178 GLTSSSVYTPSSSTPSSQVTCVSAHPASSFTVDKLEPSPGISTINPCPCCKCP 237
 DB 61 GLTSSSVYTPSSSTGLTQTYICNVHKSNTKVDKVERKSCDKI-HICPP-----CP 113
 QY 238 APNLEGPSVFTFPPIKDYLMISLTPKVTQVVDVSEDDPDVQISMFVNNVEVHTAQTO 297
 DB 114 APELLGSPSVFTFPKPKDTLMISRPEVTQVVDVSHEDPEVKFMVYDGEVHNAKTK 173
 QY 298 THREDNSTIRVSTLPPIOHOMMSGKEFKCKYNNKDLSPERTISKIGLVRAQYVI 357
 DB 174 PREQYNSYTRVSVLTVAHQDLNKEKCYKSNALPAPLEKTSKAKGPREQYVT 233
 QY 358 LPPAPQLSRKDYSLTCLVGVGFNPDISVEWTSNGHTEENYKDTAVLDSDSYFTSKL 417
 DB 234 LPPSRBELTKNQVSLTCLVKGFPSPDIAYEMESNGPENNKTTPVLDSDGSFLYSKL 293
 QY 418 NMKTSKWEKTDSEFCNVRHREGLKNYLAKTISRSPGK 454
 DB 294 TVDKSRMOQGNVFFSCVMHEALHNHYTKSLSPGK 330
 RESULT 15
 GC_RABIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE IG GAMMA CHAIN C REGION.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84030930; PubMed-6313520;
 RA Bernstein K.E., Alexander C.B., Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 RL F-I haplotype."
 RL Immunogenetics 18:387-397(1983).
 RN [2]
 RP SEQUENCE OF 1-128.
